

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/027,277

DATE: 01/15/2002
TIME: 08:09:24

Input Set : A:\ES.txt
Output Set: N:\CRF3\01152002\J027277.raw

ENTERED

3 <110> APPLICANT: Benson, Timothy
4 Durbin, Jim
5 Prince, D. Bryan
7 <120> TITLE OF INVENTION: CRYSTALLIZATION AND STRUCTURE DETERMINATION OF GLYCOSYLATED
HUMAN BETA
8 SECRETASE, AN ENZYME IMPLICATED IN ALZHEIMER'S DISEASE
10 <130> FILE REFERENCE: 00481 CN1
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/027,277
13 <141> CURRENT FILING DATE: 2001-12-21
15 <150> PRIOR APPLICATION NUMBER: 09/808,262
16 <151> PRIOR FILING DATE: 2001-03-14
18 <150> PRIOR APPLICATION NUMBER: 09/747,420
19 <151> PRIOR FILING DATE: 2000-12-23
21 <160> NUMBER OF SEQ ID NOS: 5
23 <170> SOFTWARE: PatentIn version 3.0
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 385
27 <212> TYPE: PRT
28 <213> ORGANISM: Homo sapiens
30 <400> SEQUENCE: 1
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33 1 5 10 15
35 Glu Met Thr Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp
36 20 25 30
38 Thr Gly Ser Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu
39 35 40 45
41 His Arg Tyr Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg
42 50 55 60
44 Lys Gly Val Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu
45 65 70 75 80
47 Gly Thr Asp Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg
48 85 90 95
50 Ala Asn Ile Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly
51 100 105 110
53 Ser Asn Trp Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg
54 115 120 125
56 Pro Asp Asp Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr
57 130 135 140
59 His Val Pro Asn Leu Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro
60 145 150 155 160
62 Leu Asn Gln Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile
63 165 170 175
65 Gly Gly Ile Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro
66 180 185 190
68 Ile Arg Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile
69 195 200 205
71 Asn Gly Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys
72 210 215 220

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74 Ser Ile Val Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val
75 225      230      235      240
77 Phe Glu Ala Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys
78      245      250      255
80 Phe Pro Asp Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala
81      260      265      270
83 Gly Thr Thr Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met
84      275      280      285
86 Gly Glu Val Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln
87      290      295      300
89 Tyr Leu Arg Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr
90 305      310      315      320
92 Lys Phe Ala Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val
93      325      330      335
95 Ile Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile
96      340      345      350
98 Gly Phe Ala Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala
99      355      360      365
101 Ala Val Glu Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr
102      370      375      380

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104 Asn

105 385

107 <210> SEQ ID NO: 2

108 <211> LENGTH: 21

109 <212> TYPE: PRT

C--> 110 <213> ORGANISM: Artificial

112 <220> FEATURE:

113 <223> OTHER INFORMATION: Histidine Tag

115 <400> SEQUENCE: 2

117 Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Met His Thr Glu His

118 1 5 10 15

120 His His His His His

121 20

123 <210> SEQ ID NO: 3

124 <211> LENGTH: 13

125 <212> TYPE: PRT

C--> 126 <213> ORGANISM: Artificial

128 <220> FEATURE:

129 <223> OTHER INFORMATION: Synthetic Peptide

131 <220> FEATURE:

132 <221> NAME/KEY: MOD_RES

133 <222> LOCATION: (5)..(5)

134 <223> OTHER INFORMATION: Statine

137 <400> SEQUENCE: 3

DK> 139 Ser Glu Val Asn Xaa Val Ala Glu Phe Arg Gly Gly Cys

140 1 5 10

142 <210> SEQ ID NO: 4

143 <211> LENGTH: 32

144 <212> TYPE: DNA

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C--> 145 <213> ORGANISM: Artificial

147 <220> FEATURE:

148 <223> OTHER INFORMATION: Primer

150 <400> SEQUENCE: 4

151 cgctttggat ccgtggacaa cctgaggggc aa

32

154 <210> SEQ ID NO: 5

155 <211> LENGTH: 40

156 <212> TYPE: DNA

C--> 157 <213> ORGANISM: Artificial

159 <220> FEATURE:

160 <223> OTHER INFORMATION: Primer

162 <400> SEQUENCE: 5

163 cgctttggta ccctatgact catctgtctg tggaatgttg

40

VERIFICATION SUMMARY

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L:110 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:2
L:126 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:3
L:139 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:145 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4
L:157 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5